Critical properties of the susceptible-exposed-infected model on a square lattice

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Abstract.
The critical properties of the stochastic susceptible-exposed-infected model on a square lattice is studied by numerical simulations and by the use of scaling relations. In the presence of an infected individual, a susceptible becomes either infected or exposed. Once infected or exposed, the individual remains forever in this state. The stationary properties are shown to be the same as those of isotropic percolation so that the critical behavior puts the model into the universality class of dynamic percolation.

1. Introduction

Spatio-temporal structures as well as fluctuations are essential features of epidemic spreading [1, 2, 3, 4]. A description of epidemic spreading that takes into account these essential features is provided by stochastic lattice models [5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16] in which each site of a lattice is occupied by an individual that can be in one of a certain number of states. In the susceptible-infected-recovered (SIR) model [13, 14, 15], an important model in this context, the possible states are susceptible (S), infected (I) or recovered (R). The SIR model is composed by two processes. One in which a susceptible becomes infected by a catalytic reaction, S+I→I+I, and another in which an infected becomes recovered spontaneously, I→R. Another model, the one that will be the object our study here, is the susceptible-exposed-infected (SEI), introduced by Tomé and de Oliveira [15], in which each individual can be susceptible (S), exposed (E) or infected (I). This model has also two processes. In the presence of an infected individual, a susceptible individual may become either infected or exposed, processes represented by the reactions S+I→I+I and S+I→E+I, respectively.

The distinguish features of these two models are as follows. The spreading of the epidemic occurs as long as there are active sites, which are the sites occupied by a susceptible individual next to an infected individual. When the active sites have disappeared, the infection reaction S+I→I+I no longer takes place, that is, no new infected individuals are created, and the whole process eventually stops. The system finds itself in one of many absorbing states which, in the SIR model, are the configurations formed by R and S sites and, in the SEI model, are the configurations without any pair of neighboring SI sites. Starting from a configuration full of susceptible individuals except for a single infected site, the process generates a cluster of inactive sites, which are the R sites of the SIR model and the I sites of the SEI model. In the stationary state, which is an absorbing state, these clusters have the same properties as the clusters occurring in isotropic percolation model so that the stationary properties of these two models are similar to percolation.

When the rate of infection is small there is no epidemic spreading, that is, the generated clusters are all finite. If however the infection rate is large enough, an infinite cluster of inactive sites is generated and the epidemic spreading takes place. The transition from non-spreading to spreading is regarded as a continuous phase transition with critical behavior within the universality class of dynamical percolation [9, 10, 11, 12, 13, 14, 17, 18, 19, 20]. In fact, the clusters generated by the rules of the SEI model can be exactly mapped into the clusters of site percolation so that the stationary properties of the SEI model are identical to the properties of site percolation. In this sense, it is similar to the model introduced by Alexandrowicz [21] to generate percolation clusters. The SEI model can thus be regarded as a standard example of a model belonging to the dynamical percolation universality class. Here we are concerned with the critical behavior of the SEI model on a square lattice, particularly with the numerical calculation of the dynamic critical exponents. As to the static critical

exponents, they are the same as the percolation in two dimensions and known exactly [22]. Here we perform calculation for the SEI model with results for the dynamic critical exponents that are very accurate, and in agreement with the exponents of the dynamic percolation universality class [13, 20].

2. Model

The SEI model is a continuous time stochastic markovian process defined on a lattice where each site can be in one of three states: S, I or E. The allowed transitions are those in which just one site changes its state. The transition rate of the process S→I is bf, where f is the fraction of I sites in the neighborhood of the site to be updated and b is the infection parameter. The transition rate of the process S→E is af, where a is the exposition parameter. Other transitions are forbidden so that sites in states I or E remain forever in these states. For convenience, we define the parameters $p = b/(a + b)$ and $q = a/(a + b)$ so that $p + q = 1$. The model displays two regimes. One in which there is no epidemic spreading, occurring for small infection rate, and the other in which the epidemic spreading takes place, occurring for large infection rate. The stationary properties are close related to site percolation model. In fact, the cluster of I sites can be exactly mapped into the cluster of site percolation in the same lattice, in which each site is occupied with probability p, as will be shown below. It is well known that the percolation model [22] shows a phase transition from a state with finite clusters, occurring for $p < p_c$, to a state with an infinite cluster, or percolating state, for $p > p_c$, where p_c is the critical concentration. We thus expect for the SEI model, a transition from a non-spreading regime, for $p < p_c$, to a spreading regime, for $p > p_c$.

The simulation of the model is carried out as follows. Each site of a regular lattice with N sites can be in one of three states: occupied by a susceptible (S), by an infected (I) or by an exposed (E) individual. At each time step a site is chosen at random. If it is in the I or E states nothing happens. If it is in the state S then with probability pf it becomes I and with probability qf it becomes E, where f is the fraction of I sites in the neighborhood of the chosen site and $p + q = 1$. Equivalently, if the chosen site is in state S, we may randomly choose a neighboring site; if it is in the I state then the chosen site becomes I with probability p or E with the complementary probability $q = 1 - p$. The time is increased by an amount equal to $1/N$. The neighborhood of a site is defined as its nearest neighbor sites.

An alternative approach, useful for time dependent simulations, is carried out as follows. At each time step, a site is chosen at random from a list comprising the I sites only. Next, one of its neighbors is chosen at random. If this neighbor is in state I or E nothing happens. If it is in state S, then it changes to I with probability p or to E with probability $q = 1 - p$. The time is increased by an amount equal to $1/n_I$ where n_I is the number of sites in the list, which is the total number of I sites in the lattice, and the list is updated. An even more efficient algorithm is set up by using a list of active pair of sites, more precisely, a list of nearest neighbor pairs of susceptible-infected sites. At

each time step, a pair of the list is chosen at random and the S site of the pair becomes I with probability p or E with probability $q = 1 - p$. The time is increased by an amount $1/n_{SI}$ where n_{SI} is the number of entries in the list, which is the total number of SI pairs in the lattice, and the list is updated.

Let us consider a finite lattice full of susceptible individual except for one site which is occupied by an infected individual. The system evolves in time and eventually reaches its final state which comprises a connected cluster of infected sites in addition to exposed and susceptible sites. The exposed sites are found at the boundary of the cluster separating the infected sites from the susceptible sites, so that active sites are absent. The clusters generated by the SEI rules are the same clusters of site percolation, as we show next, in which the sites are occupied independently with probability p.

The mapping of the stationary properties of the SEI model into the site percolation model can be understood as follows. Suppose that a cluster C of infected sites of a lattice has been generated by one of the algorithm above, starting from an infected site at the origin. Suppose moreover that the dynamics has come to a halt so that there are no pairs of the type SI. The boundary B of this cluster is therefore composed only by E sites. During the dynamics, whenever the site i becomes either I or E, we keep the used random number ξ_i. It is clear that, if site i has turned into an I site then $\xi_i \leq p$; if site i has turned into an E site then $\xi_i > p$. Let us now consider a replica of the lattice, with all sites empty except the site at the origin which is occupied. Next the site i of the replica is occupied if $\xi_i \leq p$ and remains empty if $\xi_i > p$. By means of this procedure, which is the procedure used in site percolation, a cluster of occupied sites is generated, which is thus identical to the cluster of I sites of the original lattice.

3. Scaling relations

Around the critical point, the quantities that characterize the system are assumed to obey a scaling relation. We assume two types of scaling relation. The first one is a finite-size scaling relation, valid at the stationary state. A certain quantity Q depends on the linear size of the system L and on the deviation $\varepsilon = p - p_c$ according to

$$Q(\varepsilon, L) = L^{x/\nu_\perp} \Phi(\varepsilon L^{1/\nu_\perp}), \tag{1}$$

where $\nu_\perp$ is the critical exponents related to the spatial correlation length and x is the critical exponent related to Q in the thermodynamic limit, that is, $Q \sim \varepsilon^{-x}$ when $L \to \infty$. The second type is a time dependent scaling relation, valid for an infinite system, and given by

$$Q(\varepsilon, t) = t^{x/\nu_\parallel} \Psi(\varepsilon t^{1/\nu_\parallel}), \tag{2}$$

where $\nu_\parallel$ is the critical exponents related to the time correlation length. When $t \to \infty$, we get the same behavior $Q \sim \varepsilon^{-x}$. At the critical point, relations (1) and (2) predict the following scaling forms

$$Q \sim L^{x/\nu_\perp}, \qquad Q \sim t^y, \tag{3}$$

respectively, where $y = x/\nu_\parallel$.

The behavior of the SEI model is characterized by a set of quantities. We define the average $N_I = \langle n_I \rangle$ where n_I is the number of infected sites and the average $N_{SI} = \langle n_{SI} \rangle$ in the number of active pair of sites defined as the number n_{SI} of pairs of neighboring sites of type SI. Another relevant quantity is the surviving probability $P(t)$, defined as the probability that at time t the system is active, that is, as long $n_{SI} \neq 0$. Starting from one infected site in a infinite lattice full of susceptible, we expect the following asymptotic time behavior, at the critical point,

$$N_I(t) \sim t^\eta, \tag{4}$$

$$N_{SI}(t) \sim t^\theta, \tag{5}$$

$$P(t) \sim t^{-\delta}, \tag{6}$$

$$\xi(t) \sim t^{1/z}. \tag{7}$$

where ξ is the spatial correlation length and $z = \nu_\parallel/\nu_\perp$.

If several trials are carried out, some survive up to time t, some do not. In the limit $t \to \infty$, the cluster of a surving trial will be identified with the infinite percolating cluster. Let n_s be the variable that counts the number of infected sites in the surviving trials. Denoting by M and M_s the number of trials and the number of surviving trials, respectively, and by n_{si} the number of infected sites in the i-th surviving trial, then the average N_s of n_s over the surving trials is given by

$$N_s = \frac{1}{M_s} \sum_i n_{si} = \frac{M}{M_s} \left(\frac{1}{M} \sum_i n_{si} \right). \tag{8}$$

The quantity between parentheses, which we denote by N_I', is the average number of n_s over all trials because $n_s = 0$ for a nonsurviving trial. Taking into account that $P = M_s/M$ then $N_s = N_I'/P$. Now, the quantity N_I' has a behavior similar to the average N_I of n_I over all trials. In fact, we found numerically that N_I' is proportional to N_I for large enough t. Therefore, for large enough t we may write $N_s \sim N_I/P$. Taking into account relations (4) and (6),

$$N_s(t) \sim t^{\eta+\delta}. \tag{9}$$

The number of infected sites in surviving trials inside a region of linear size ξ is proportional to the order parameter P. This amounts to say that the ratio N_s/ξ^d is proportional to P. Writing thus $N_s/\xi^d \sim P$, and taking into account relations (6), (7) and (9), we reach the following exponent relation

$$z(\eta + 2\delta) = d. \tag{10}$$

At the critical point a surviving trial, which makes up the percolating cluster, has a fractal structure with a fractal dimension d_F defined by
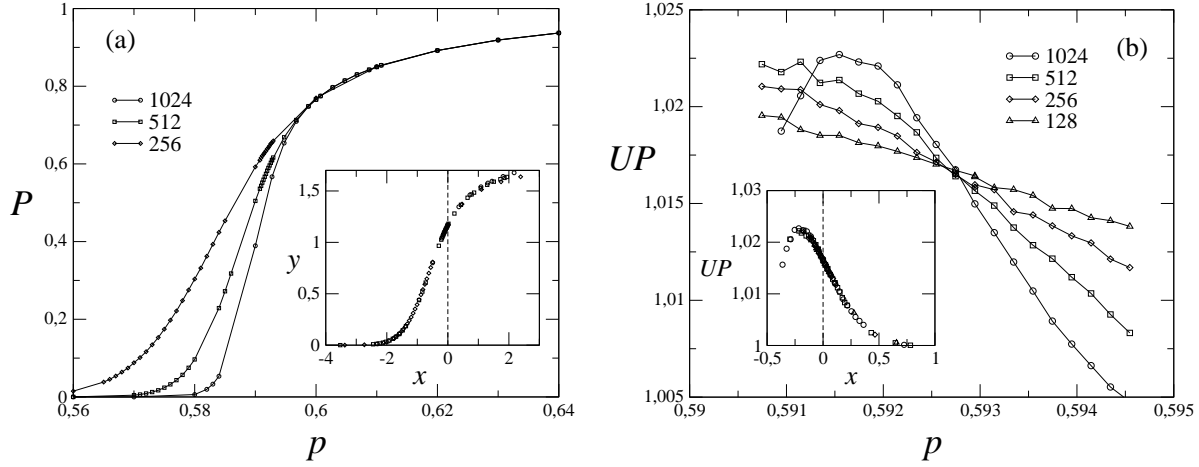
$$N_s \sim \xi^{d_F}. \tag{11}$$

Figure 1. Static properties of the SEI model from numerical simulations on a square lattice. (a) Order parameter P versus p for several values of L indicated. The inset is a data collapse showing $y = PL^{\beta/\nu_\perp}$ versus $x = \varepsilon L^{1/\nu_\perp}$ where $\varepsilon = p - p_c$. (b) The quantity UP versus p for several values of L indicated. The inset is a data collapse showing UP versus x.

Comparing (7) and (9) with (11), we see that the fractal dimension d_F of the critical cluster is related to η and δ by

$$z(\eta + \delta) = d_F. \tag{12}$$

The exponents θ and η are connected by the relation

$$\eta = 1 + \theta, \tag{13}$$

which can be understood by observing that the rate of increase in the average number of infected sites is proportional to the number of active pair of sites, that is,

$$\frac{d}{dt}N_I = \frac{b}{k}N_{SI} \tag{14}$$

where k is the number of neighbors. Replacing (5) into (14), it follows that $N_I \sim t^{1+\theta}$ from which we find relation (13). We should remark that in models belonging to direct percolation (DP) universality class [12], $N_I \sim N_{SI}$ so that the exponents η and θ coincide. In the case of models belonging to dynamical percolation universality class, such as the SIR and SEI models, they are distinct and are related by (13).

When $t \to \infty$, that is, in the stationary state, the surviving probability, which is identified with the order parameter, behaves around the critical point as

$$P \sim \varepsilon^\beta \tag{15}$$

and the exponent β is related to δ by

$$\delta\nu_\parallel = \beta, \tag{16}$$

which is equivalent to $\delta z = \beta/\nu_\perp$. Taking into account this relation and comparing relations (12) and (10), we find $\eta z = \gamma/\nu_\perp$, where $\gamma = d\nu_\perp - 2\beta$, and $(d - d_F)\nu_\perp = \beta$.
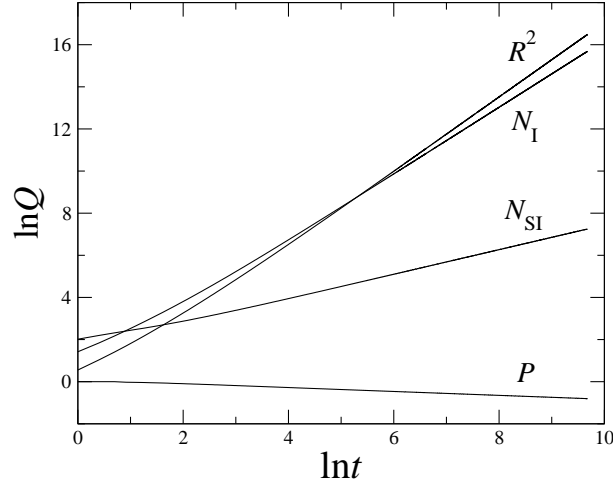
Figure 2.   Number of infected sites N_I, number of active pair of sites N_{SI}, surviving probability P and spreading of the infected sites R^2 as a function of time t in a double-log plot. The slopes of the curves for large enough time give, respectively, η, θ, $-\delta$ and $2/z$.

The density ρ of infected sites is equal to to N_I/N. Bearing in mind that $N_I = N_s P$ and that $N_s = PN$, we conclude that $\rho \sim P^2$ so that

$$\rho \sim \varepsilon^{2\beta}. \tag{17}$$

Let us define the quantity $\rho_2 = \langle n_I^2 \rangle / N^2$. Taking into account that $\langle n_s^2 \rangle = \langle n_I^2 \rangle / P$ and that $\langle n_s^2 \rangle / N^2 \sim P^2$ around the critical point, we may conclude that $\rho_2 \sim P^3$, or

$$\rho_2 \sim \varepsilon^{3\beta}. \tag{18}$$

The quantity U, defined as the ratio $U = \langle n_I^2 \rangle / \langle n_I \rangle^2 = \rho_2/\rho^2$ behaves as

$$U \sim \varepsilon^{-\beta}. \tag{19}$$

Scaling relations can be written for the quantities defined above. For instance, the order parameter obeys the scaling relation

$$P(\varepsilon, L) = L^{-\beta/\nu_\perp} \Phi_1(\varepsilon L^{1/\nu_\perp}). \tag{20}$$

From the above relations for U and P, it follows that the product UP approaches a constant at the critical point and obeys the relation [14]

$$UP = \Phi_2(\varepsilon^{\nu_\perp} L), \tag{21}$$

so that, at the critical point, $\varepsilon = 0$, a plot of UP versus p for several values of L will cross at the same point, the critical point.

4. Simulations

We performed numerical simulation on a square lattice by using the algorithms explained above. The stationary properties were obtained on lattices of several sizes, and for several values of the parameter p. The order parameter P was obtained as follows [14].

We perform several runs starting from an infected individual placed in the center of a finite lattice full of susceptible individuals. The quantity $P(p, L)$ is the fraction of runs such that an infected individual reaches the border of the lattice of linear size L. In figure 1a we show the order parameter P versus p for several values of L. The inset of figure 1a shows a data colapse according to the scaling form (20). To get the data colapse we used the exact values of the percolation exponents in two dimensions [22]: $\beta = 5/36$ and $\nu_\perp = 4/3$. We used also the numerical value of p at the critical point on a square lattice, $p_c = 0.59274606(5)$ obtained from Monte Carlo simulations [23].

In figure 1b, we show the product UP as a function of p. As expected from scaling relation (21) the curves for distinct L cross at the critical point. The value of UP at p_c is estimated to be $(UP)_c = 1.01658(1)$, which is a linear extrapolation in $1/L^2$ obtained from the values 1.016598, 1.016585, 1.016582 of this quantity for $L = 256, 512, 1024$ respectively. The quantity UP at p_c is a universal quantity and may be compared to the values 1.0167(1) obtained for percolation and SIR models [14]. The inset of figure 1b shows the data collapse according to (21). Again we use the exact value $\nu_\perp = 4/3$.

To get the dynamic exponents defined by relations (4), (5), (6), (7), we performed time-dependent Monte Carlo simulations at the critical point $p_c = 0.59274606(5)$ [23]. To get the exponents η, θ and δ, we have estimated the number of infected sites N_I, the number of active pair of sites N_{SI} and the surviving probability P. The exponent z was obtained by calculation the spreading of the infected sites R^2 [7], defined by

$$R^2 = \frac{1}{N_I} \sum_i r_i^2 \langle \eta_i \rangle \tag{22}$$

where r_i is the distance of site i to the origin and η_i takes the value 1 when site i is occupied by an infected individual and zero otherwise. At the critical point

$$R^2 \sim t^{2/z}. \tag{23}$$

Figure 2 shows the quantities N_I, N_{SI}, P and R^2 as a function of time. Each curve corresponds to an average over 10^6 runs obtained on a square lattice of linear size $L = 2^{15}$. At each run, the lattice was full of susceptible sites except the central site, which is in an infected state. Up to the maximum time shown in figure 2 no infected site reached the border of the lattice, which amounts to say that the results shown in figure 2 are valid for an infinite lattice. We remark that the quantity N_I' was also calculated and we found $cN_I' = N_I$ for large enough t, as we have assume above, and that at the critical point $c = 1.025(5)$.

To estimate the exponent y for a given quantity $Q \sim t^y$, we used a correction to scaling of the form [7]

$$Q(t) = t^y(c_1 + c_2 t^{-\mu}). \tag{24}$$

The fitting of this form to the data points gives the exponent y and μ in addition to the constants c_1 and c_2. The fitting was done within a certain interval of time starting at time t_0 and ending at time t_1. We have found that the best fittings give μ around 1, but the actual values found for the exponent y are not too sensitive to the value of the

Table 1. Critical exponents obtained by fitting the scaling form (4) to the curves in figure 2 within the time interval between t_0 and t_1. The last row gives the average of the values in the previous rows, together with the errors in the last digit.

$\ln t_0$	$\ln t_1$	η	θ	δ	z
4.5	9.5	1.58462	0.58444	0.09217	1.13096
5.5	9.5	1.58457	0.58438	0.09208	1.13087
6.5	9.5	1.58454	0.58442	0.09196	1.13083
		1.5846(2)	0.5844(2)	0.0921(3)	1.1309(3)

exponent μ. We used three values of t_0 and the same value of t_1. As seen in table 1, the three values of a given exponent are distinct but very similar allowing the estimation of the statistical error shown in the last row together with the average.

The estimated exponents can be checked by using relations $\eta z = \gamma/\nu_\perp$ and $\delta z = \beta/\nu_\perp$. From the values of η and z we get $\eta z = 1.7920(7)$ which should be compared with the exact result $\gamma/\nu_\perp = 43/24 = 1.791666\ldots$ [22]. From the values of δ and z we get $\delta z = 0.1042(4)$ which should be compared with the exact result $\beta/\nu_\perp = 5/48 = 0.104166\ldots$ [22]. We remark that our results are in agreement with results for the exponents of models belonging to the universality class of dynamic percolation [13, 20]. Notice that the critical exponents η and θ satisfy, within the statistical error, the relation (13), $\eta = 1 + \theta$.

5. Discussion

We have determined the critical properties of the SEI model on a square lattice by numerical simulations. The model is an example of model belonging to the universality class of dynamical percolation. The stationary properties are shown to be exactly the same as those of isotropic percolation, so that the static exponents are the same as percolation, which in two dimensions are known exactly. This is not the case of the dynamic exponents which we have calculated here by using a time-dependent simulations. Our numerical estimation, within the statistical errors, are in good agreement with the known relations among the exponents. An important feature that distinguish this model from models belonging to the DP universality class [12], such as the susceptible-infected-removed-susceptible (SIRS) [13], rests on the relation between the number of infected sites and the number of active pairs of sites. In the SIRS model these two quantities are closed related leading to the identification of the exponents η and θ. In the SEI model they are distinct leading to the relation $\eta = 1 + \theta$, which was confirmed by our numerical simulations.

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